CLAIMS

1. Method for the acquisition of a mass spectrum containing information about sequences of a biopolymer using a tandem mass spectrometer with an ion source for an ionization of the biopolymer by means of matrix-assisted laser desorption, the method comprising:

generating in-source decay (ISD) fragment ions of the biopolymer using high laser energy density in the ion source;

selecting and subjecting one species of the fragment ions to a further fragmentation by means of gas collisions (CID), surface collisions (SID), photon collisions (PID) or metastable decay (LID) to form granddaughter ions; and

measuring the granddaughter ions as a mass spectrum.

2. Method according to Claim 1 wherein the tandem mass spectrometer is a tandem in time mass spectrometer.

3. Method according to Claim 1 wherein the tandem mass spectrometer is a tandem in time mass spectrometer.

4. Method according to Claim 3, wherein the tandem in space mass spectrometer comprises magnetic sector mass spectrometers, quadrupole filter mass spectrometers, ion trap mass spectrometers or time-of-flight mass spectrometers.

5. Method for the acquisition of a mass spectrum containing information about sequences of a biopolymer, in a tandem mass spectrometer with an ion source for the ionization of the biopolymer by means of matrix-assisted laser desorption, the method comprising:

(a) preparing the biopolymer together with a matrix substance as a sample on a sample support;

(b) placing the sample support in the ion source;

(c) bombarding the sample on the sample support with light pulses from a pulsed laser with such a high energy density that it causes spontaneous fragmentations of a part of the biopolymer molecules whereby different types of ISD fragment ions are formed;
(d) accelerating the ions and injecting them into the first mass spectrometer of a tandem mass spectrometer;
(e) selecting one species of ISD fragment ion in the first mass spectrometer and fragmenting these selected ions at least partially to granddaughter ions; and
(f) measuring the granddaughter ions in the second mass spectrometer of the tandem mass spectrometer to form a mass spectrum.

6. Method according to Claim 5, wherein the tandem mass spectrometer comprises a quadrupole filter and a time-of-flight mass spectrometer with orthogonal ion injection.

7. Method according to Claim 5, wherein the tandem mass spectrometer comprises two coaxially aligned time-of-flight mass spectrometers (TOF/TOF).

8. Method according to Claim 7, wherein the fragmentation of the ISD fragment ions to granddaughter ions in the first time-of-flight mass spectrometer is caused by collisional fragmentation (CID) or metastable decay (LID).

9. Method according to Claim 5, wherein the spectrum acquisition of the granddaughter ions is preceded by a spectrum acquisition of the ISD fragment ions generated in the ion source by the laser bombardment and wherein the spectrum of the ISD fragment ions serves to select the ISD fragment ions for the spectrum acquisition of the granddaughter ion spectra.

10. Method according to Claim 9, wherein the biopolymers are proteins and wherein to assist in the selection of the ISD fragment ions, spectrum acquisitions of the ISD fragment ions with different matrix substances are used.

11. Method according to Claim 9, wherein the biopolymers are proteins and prior to a spectrum acquisition the cross links of the proteins are dissolved.

12. Method according to Claim 11, wherein disulfide bridges between cysteines are dissolved by reduction and alkylation, or by oxidation.

13. Method for the determination of the terminal sequences of a protein wherein granddaughter ion spectra of different types of ISD fragment ion of the same fragmentation series are acquired, the method comprising:

comparing the granddaughter ion spectra to determine the terminal ion series of the ISD fragment ions, whereby the ion series are identified by the fact that one ion fragmentation series in the granddaughter ion spectra is fixed in the spectra while the other ion series appears to be shifted from spectrum to spectrum; and

using the mass differences of the fixed fragmentation series to read out the terminal sequence pattern of the protein from the terminal ion series.

14. Method according to Claim 13, wherein a computer program is used to identify the terminal ion series from the measuring data of the granddaughter ion spectra.

15. Method according to Claim 14, wherein the determination of the sequence pattern is also performed by means of a computer program.